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available
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NEWS EXPRESS MARCH 31 CURRENT WINDOWS VERSION IS V7.00A, CURRENT
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L4 ANSWER 6 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Identification and cloning of plant sterol biosynthetic enzymes

L4 ANSWER 7 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
 TI **Isolation** and cloning of corn NADH dehydrogenase genes and their role in disease resistance

L4 ANSWER 8 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Identification and cloning of plant thiamine biosynthetic enzymes

L4 ANSWER 9 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
 TI **Rice** regulatory sequences for gene expression in defined wheat monocotyledonous tissue

L4 ANSWER 10 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Cloning and characterization of **rice** RH3 gene induced by brown planthopper

=> d 3 ab

L4 ANSWER 3 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
 AB Methods for **isolation** and use of regulatory sequences from corn and wheat for selective control of gene expression in male reproductive tissue are presented. Comparative anal. of corn or wheat anther tissue cDNA **libraries**, relative to that of other tissues, identified anther-specific gene expression patterns and resp. gene regulatory sequences. Plasmid expression vectors were created containing these regulatory sequences, a minimal promoter (CaMV 35S or **rice** actin gene), and a reporter gene (GUS gene encoding β -glucuronidase). Male reproductive tissue-specific expression in both monocots and dicots was identified following transfer of recombinant plasmid vector to corn, wheat, **rice** and Arabidopsis thaliana. These promoters can be used in plants to regulate transcription of target genes including genes for control of fertility, insect or pathogen tolerance, herbicide tolerance or any gene of interest.

=> d 3 so

L4 ANSWER 3 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
 SO U.S. Pat. Appl. Publ., 62 pp.
 CODEN: USXXCO

=> d 11-20 ti

L4 ANSWER 11 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1
 TI Transcriptome study in the Chinese human **genome** project

L4 ANSWER 12 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
 TI **Isolation** and expression analysis of salt stress-associated ESTs from contrasting **rice** cultivars using a PCR-based subtraction method

L4 ANSWER 13 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 2
 TI Analysis of the transcriptional response to **Rice** Yellow Mottle Virus infection in Oryza sativa indica and japonica cultivars

L4 ANSWER 14 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 3
 TI Serial Analysis of Gene Expression (SAGE) of Magnaporthe grisea: genes involved in appressorium formation

L4 ANSWER 15 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN

- TI A comparative study of genetic relationships among the AA-genome
Oryza species using RAPD and SSR markers
- L4 ANSWER 16 OF 48 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
TI Efficient preparation and sequencing of BAC shotgun **libraries**,
BAC ends, and ESTs.
- L4 ANSWER 17 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
TI Sequence of plant protein CHD and uses in transformation of plant to
induce somatic embryogenesis and apomixis
- L4 ANSWER 18 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
TI Corn auxin-responsive transcriptional regulatory element and axig1
polynucleotides and methods of altering gene expression in plants
- L4 ANSWER 19 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
TI Plant genes encoding vitamin B metabolism proteins
- L4 ANSWER 20 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
TI Identification and cloning of plant sugar transport protein cDNA

=> d 12 ab

- L4 ANSWER 12 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
AB Salt stress adversely affects the growth of **rice** plants. To
understand the mol. basis of salt-stress response, four subtracted cDNA
libraries were constructed employing specific NaCl-stressed
tissues from salt-tolerant (CSR 27 and Pokkali) and salt-sensitive (Pusa
basmati 1) **rice** cultivars. An efficient PCR-based cDNA
subtraction method was employed for the **isolation** of the
salt-stress responsive cDNA clones. In all, 1266 cDNA clones were
isolated in the course of this study, out of which 85 clones were
end-sequenced. Database search of the sequenced clones showed that 22
clones were homologous to genes that have earlier been implicated in
stress response, 34 clones were novel with respect to their function and
six clones showed no homol. to sequences in any of the public database.
Northern anal. showed that the transcript expression pattern of selected
clones was variable amongst the cultivars tested with respect to
stress-regulation.

=> d 12 so

- L4 ANSWER 12 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
S0 Theoretical and Applied Genetics (2003), 106(4), 620-628
CODEN: THAGA6; ISSN: 0040-5752

=> d 15 ab

- L4 ANSWER 15 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
AB In order to **est.** genetic relationships of the AA-genome
Oryza species, RAPD and SSR analyses were performed with 45 accessions,
including 13 cultivated varieties (eight Oryza sativa and five Oryza
glaberrima) and 32 wild accessions (nine Oryza rufipogon, seven Oryza
nivara, three Oryza glumaepatula, four Oryza longistaminata, six Oryza
barthii, and three Oryza meridionalis). A total of 181 clear and
repeatable bands were amplified from 27 selected RAPD primers, and 101
alleles were detected from 29 SSR primer pairs. The dendrogram
constructed using UPGMA from a genetic-similarity matrix based on the RAPD
data supported the clustering of distinct five groups with a few
exceptions: O. rufipogon/O. nivara/O. meridionalis, O. barthii/O.
glaberrima, O. glumaepatula, O. sativa and O. longistaminata. The

dendrogram based on the SSR anal. showed a more-complicated genetic variation pattern, but the *O. longistaminata* and *O. barthii*/*O. glaberrima* accessions were consistently separated from all other accessions, indicating significant differentiation of the African AA-**genome** *Oryza* species. For accessions in the *O. rufipogon*/*O. nivara*/*O. sativa* complex, it is apparent that geog. **isolation** has played an important role in differentiation of the Asian AA-**genome** *Oryza* taxa. It is also demonstrated from this study that both RAPD and SSR analyses are powerful methods for detecting polymorphisms among the different AA-**genome** *Oryza* accessions. However, the RAPD anal. provides a more-informative result in terms of the overall genetic relationships at the species level compared to the SSR anal. The SSR anal. effectively reveals diminutive variation among accessions or individuals within the same species, given approx. the same number of primers or primer-pairs used in the studies.

=> d 15 so

L4 ANSWER 15 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
SO Theoretical and Applied Genetics (2003), 108(1), 113-120
CODEN: THAGA6; ISSN: 0040-5752

=> d 16 ab

L4 ANSWER 16 OF 48 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AB *Magnaporthe grisea*, the causal agent of **rice** blast disease, is a major threat to **rice** production worldwide. In conjunction with several high throughput sequencing projects, we have developed BAC shotgun **library** preparation and sequencing techniques that are cost effective and avoid the use of expensive laboratory robotics. Qiagen Large Scale Construct kits yield up to 150 micrograms of clean BAC DNA void of *E. coli* genomic DNA. To generate the BAC shotgun **library**, DNA is sheared to an average fragment size of 1-2 kilobases, extracted using a Qiagen Gel **Purification** kit, blunt end repaired, ligated and transformed into *E. coli*. Samples are prepared using a modified alkaline lysis protocol in a 96 well format. Yield is typically over 4 micrograms of high quality DNA. One researcher can prepare 768 clones in four hours. The DNA is sequenced using 1/8 or 1/16 Big Dye reactions with over ninety percent sequencing success. We will present details of **library** construction and the sequencing techniques used to sequence 37 BACs and describe variations that we employ for **EST** and BAC end sequencing.

=> d 16 so

L4 ANSWER 16 OF 48 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
SO Phytopathology, (June 2003) Vol. 93, No. 6 Supplement, pp. S82. print.
Meeting Info.: Annual Meeting of the American Phytopathological Society.
Charlotte, North Carolina, USA. August 09-13, 2003. American
Phytopathological Society.
ISSN: 0031-949X (ISSN print).

=> d 21-30 ti

L4 ANSWER 21 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 4
TI Identification of the 19S regulatory particle subunits from the
rice 26S proteasome

L4 ANSWER 22 OF 48 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
TI In silico cloning of glucose-6-phosphate dehydrogenase cDNA from

rice (*Oryza sativa* L.).

- L4 ANSWER 23 OF 48 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
TI **Isolation** of conserved genes in the human testis by subtractive hybridization.
- L4 ANSWER 24 OF 48 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN
TI A comprehensive **rice** transcript map containing 6591 expressed sequence tag sites. DUPLICATE 5
- L4 ANSWER 25 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
TI Plant defense induced genes encoding multidrug resistance efflux protein and uses in improving plant disease resistance
- L4 ANSWER 26 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
TI Identification of defense-related **rice** genes by suppression subtractive hybridization and differential screening
- L4 ANSWER 27 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
TI Construct design for efficient, effective and high-throughput gene silencing in plants
- L4 ANSWER 28 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
TI Micron, a microsatellite-targeting transposable element in the **rice genome**
- L4 ANSWER 29 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
TI **Isolation** of candidate genes for tolerance of abiotic stresses
- L4 ANSWER 30 OF 48 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN
TI Mapping genes on an integrated sorghum genetic and physical map using cDNA selection technology. DUPLICATE 6

=> d 26 ab

- L4 ANSWER 26 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
AB Identification of host genes involved in defense responses is one of the most critical steps leading to the elucidation of disease resistance mechanisms in plants. In this study, two different cloning strategies were employed to identify defense-related genes from a tropical japonica **rice** cultivar (*Oryza sativa* cv. Drew). Differential screening of a blast fungus (*Pyricularia grisea*)-induced **rice** cDNA **library** using bacterial colony arrays led to the **isolation** of 22 distinct **rice** genes that are expressed differentially in response to blast infection. Sequence anal. indicates that most of them are full-length cDNAs encoding pathogenesis-related proteins or other relatively abundant proteins. **Rice** seedlings were treated with a combination of cycloheximide plus jasmonic acid (JA) or benzothiadiazole (BTH), followed by PCR-based suppression subtractive hybridization, in order to search for immediate early (IE) defense-related genes whose transcription is independent of de novo protein synthesis. The initial screening of only 768 subtracted clones resulted in the identification of 34 distinct IE genes that are induced by JA, BTH, and/or blast infection. Database searches revealed that these IE genes encode putative mitogen-activated protein kinase, diacylglycerol kinase, zinc finger protein, RelA-SpoT protein, ankyrin-containing protein, ABC transporter, β -ketoacyl-CoA synthase, and other potential defense-signaling

components. Further characterization of these novel IE genes will likely facilitate the elucidation of defense signal transduction in **rice** plants.

=> d 26 so

L4 ANSWER 26 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
SO Molecular Plant-Microbe Interactions (2001), 14(5), 685-692
CODEN: MPMIEL; ISSN: 0894-0282

=> d 29 ab

L4 ANSWER 29 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
AB High-throughput anal. of expressed genes, achieved by cataloguing expressed sequence tags (ESTs) and monitoring hybridization patterns by microarrays, has recently become possible in **rice**. As the first results become available, the value of these technologies can be gauged. Through ESTs and microarrays, the authors can obtain a more complete view than in the past of plant gene complexity, tissue specificity, and developmental or externally affected expression patterns. In particular, **EST** and microarray analyses can have tremendous impact in plant breeding, based on accelerated identification of complex traits such as those controlling plant responses to abiotic stresses. Owing to the novelty and lack of refinement in the use of microarray technol., the authors discuss advantages and limitations. The authors demonstrate responses to salt stress in **rice** (*Oryza sativa*) monitored by microarray anal.

=> d 29 so

L4 ANSWER 29 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
SO Rice Genetics IV, [Proceedings of the International Rice Genetics Symposium], 4th, Los Banos, Philippines, Oct. 22-27, 2000 (2001), 345-363. Editor(s): Khush, G. S.; Brar, D. S.; Hardy, B. Publisher: Science Publishers, Inc., Enfield, N. H.
CODEN: 69CFM6; ISBN: 1-57808-167-X

=> d 31-40 ti

L4 ANSWER 31 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
TI Computational and experimental characterization of physically clustered simple sequence repeats in plants

L4 ANSWER 32 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 7
TI Molecular cloning and characterization of a plant homologue of the origin recognition complex 1 (ORC1)

L4 ANSWER 33 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
TI Plant carotenoid biosynthesis enzymes and their encoding cDNA sequences

L4 ANSWER 34 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
TI Plant carotenoid biosynthesis enzymes and their encoding cDNA sequences

L4 ANSWER 35 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
TI Plant lycopene ϵ -cyclase and β -carotene hydroxylase and lycopene cyclase enzymes and their encoding cDNAs

L4 ANSWER 36 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
TI Cloning and cDNA sequences encoding plant acid and neutral triacylglycerol lipases

L4 ANSWER 37 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Plant phytic acid biosynthesis enzymes and their encoding cDNA sequences

L4 ANSWER 38 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Plant phytic acid biosynthesis enzymes and their encoding cDNA sequences

L4 ANSWER 39 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Cloning and cDNA sequences of multiple starch-debranching enzymes from Solanum tuberosum

L4 ANSWER 40 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Arabidopsis-**rice**: will colinearity allow gene prediction across the eudicot-monocot divide?

=> d 41-48 ti

L4 ANSWER 41 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Molecular characterization of the Arabidopsis SBP-box genes

L4 ANSWER 42 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 8
 TI Differential screening of rye-type cDNAs from a common wheat carrying the rye midget chromosomes

L4 ANSWER 43 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Phospholipase A2 enzymes from elm and **rice** and their use for genetic engineering of oilseed plants

L4 ANSWER 44 OF 48 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN DUPLICATE 9
 TI Large-scale **EST** sequencing in **rice**.

L4 ANSWER 45 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Expressed sequence tags in developing anthers of **rice** (Oryza sativa L.)

L4 ANSWER 46 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Evidence for genomic changes in transgenic **rice** (Oryza sativa L.) recovered from protoplasts

L4 ANSWER 47 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Sequencing and mapping the Arabidopsis **genome**: a weed model for real crops

L4 ANSWER 48 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Analysis of randomly **isolated** cDNAs from developing endosperm of **rice** (Oryza sativa L.): evaluation of expressed sequence tags, and expression levels of mRNAs

=> d 44 ab

L4 ANSWER 44 OF 48 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN DUPLICATE 9
 AB Large-scale cDNA analysis provides several great advantages for **genome** investigations in **rice**. **Isolated** and partially characterized cDNA clones have contributed not only to the construction of an RFLP linkage map and physical maps of the chromosomes but also to investigations of the mechanisms of expression of various

isozymes and family genes. The ultimate aim of our large-scale cDNA analysis is to catalogue all the expressed genes of this important cereal, including tissue-specific, developmental stage-specific, and stress-specific genes. As of August 1996, the **Rice Genome** Research Program (RGP) has **isolated** and partially sequenced more than 29000 cDNA clones from various tissues and calluses in **rice** (Nipponbare, a japonica variety). The sequence data were translated into amino acid sequences for the 3 possible reading frames, and the similarity of these amino acid sequences to known proteins registered in PIR were examined. About 25% of the clones had significant similarities to known proteins. Some of the hit clones showed **library**-specific distributions, indicating that the composition of the clones in each **library** reflects, to some extent, the regulation of gene expression specific to differentiation, growth condition, or environmental stress. To further characterize the cDNA clones, including unknown clones, nucleotide sequence similarities of 24728 clones were analyzed and the clones were classified into around 10000 independent groups, suggesting that around a half or one third of expressed genes in **rice** have already been captured. These results obtained from our large-scale cDNA analysis provide useful information related to gene expression and regulation in **rice**.

=> d 44 so

- L4 ANSWER 44 OF 48 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved.
(2004) on STN DUPLICATE 9
- SO Plant molecular biology, Sept 1997. Vol. 35, No. 1/2. p. 135-144
Publisher: Dordrecht : Kluwer Academic Publishers.
CODEN: PMBIDB; ISSN: 0167-4412

=> d 45 ab

- L4 ANSWER 45 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
- AB To survey the expressed sequence tags (ESTs) of early stages of anther development, a number of putative genes from cDNA clones of **rice** anthers at the uninucleate microspore stage were identified. The transcript levels during anther development were also investigated using the **isolated** cDNA clones as probes. Partial nucleotide sequences of 653 cDNA clones were determined by the automated sequence anal., and 77 cDNA clones, which occupied 11.8% of the total cDNAs, had significant similarity to nucleotide sequences registered in the databases. In the study, 17 cytosolic ribosomal protein genes were **isolated**. Among the genes, those encoding cytosolic ribosomal proteins L7, L26, L31, L39, rp21c, S5 and S19 were not well understood in higher plants. As expected from the redundancy in the cDNA **library**, the sucrose synthetase gene was highly expressed in anthers compared with shoots and roots. Several clones (S19, L3, L7a, L37a, L38 and L0) showed relatively lower transcript levels throughout anther development than those observed in shoots and roots of **rice** seedlings. With respect to the transcript levels in anthers at different developmental stages, coordinated decline of transcript accumulation from uninucleate stage to bi- and/or tri-nucleate stage was noted with the cDNA probes such as S22, L3, L7a, L31, L37a, L38 and P0, suggesting the ribosomal proteins may be involved in active translation in young anthers. The ribosomal protein gene expression seemed to be coordinately regulated during anther development.

=> d 45 so

L4 ANSWER 45 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
SO Plant Biotechnology (Tokyo) (1997), 14(1), 71-75
CODEN: PLBIF6; ISSN: 1342-4580

=> d 48 ab

L4 ANSWER 48 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
AB Using a cDNA library prepared from poly(A)+ RNA from 10-day-old rice endosperm, partial nucleotide sequences of randomly isolated clones were analyzed. A total of 153 (30.65) out of 500 cDNA clones showed high amino acid identity to previously identified genes. There was significant redundancy in cDNAs encoding prolamine and glutelin. About 21.0% of the cDNA clones were found to code for seed storage protein genes. Consequently, 37 independent genes were identified. Using cDNA clones encoding glutelin, prolamin, seed allergen, α -1,4-glucan branching enzyme, glycine-rich RNA binding protein, metallothionein, non-specific lipid-transfer protein and ubiquitin conjugating enzyme, the accumulation of mRNA during rice seed development was compared. Genes associated with seed storage protein and starch biosynthesis were expressed according to expected developmental stages. Glycine-rich RNA binding protein genes as well as metallothionein-like protein genes were highly expressed in developing seeds, but low in leaves of whole plants.

=> d 48 so

L4 ANSWER 48 OF 48 CAPLUS COPYRIGHT 2004 ACS on STN
SO Plant Molecular Biology (1995), 29(4), 685-9
CODEN: PMBIDB; ISSN: 0167-4412

=> s ((byrum j?) or (byrum, j?))/au
L5 71 ((BYRUM J?) OR (BYRUM, J?))/AU

=> s 15 and est?
L6 0 L5 AND EST?

=> s 15 and rice
L7 0 L5 AND RICE

=> s ((ruan y?) or (ruan, y?))/au
L8 639 ((RUAN Y?) OR (RUAN, Y?))/AU

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L9 10 L8 AND RICE

=> dup rem 19
PROCESSING COMPLETED FOR L9
L10 8 DUP REM L9 (2 DUPLICATES REMOVED)

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L10 ANSWER 1 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
TI Random amplified polymorphic DNA of the similar braconid wasps in cotton field and paddy field from China (Hymenoptera, Braconidae).

L10 ANSWER 2 OF 8 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Colony array-based cDNA library normalization by hybridizations of complex RNA probes and gene specific probes

L10 ANSWER 3 OF 8 CAPLUS COPYRIGHT 2004 ACS on STN
 TI Electron microscope study of **rice** seeds soaked in exogenous DNA solution

L10 ANSWER 4 OF 8 CAPLUS COPYRIGHT 2004 ACS on STN
 TI In vitro transcription from the Nectria haematococca PDA1 promoter in an homologous extract reflects in vivo pisatin-responsive regulation

L10 ANSWER 5 OF 8 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN DUPLICATE 1
 TI Bionomics and the appropriate time for chemical control of the white leafhopper *Thaia subrufa* (Motschulsky) Pest of **rice** in Chekiang Province, China.

L10 ANSWER 6 OF 8 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN DUPLICATE 2
 TI Studies on the **rice** virus vector small brown planthopper *Laodelphax striatella* Fallen.

L10 ANSWER 7 OF 8 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN
 TI Studies on **rice** dwarf virus disease. I. Infection, disease development and control Insect vector, *Nephotettix cincticeps*, China.

L10 ANSWER 8 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 TI STUDIES ON THE APPLICATION OF THE REVERSED PASSIVE CARBON AGGLUTINATION TEST FOR THE DETECTION OF VIRULIFEROUS **RICE** DWARF VIRUS.

=> s ((wallick k?) or (wallick, k?))/au
 L11 8 ((WALLICK K?) OR (WALLICK, K?))/AU

=> dup rem l11
 PROCESSING COMPLETED FOR L11
 L12 5 DUP REM L11 (3 DUPLICATES REMOVED)

=> d 1-5 ti

L12 ANSWER 1 OF 5 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 TI Cystic fibrosis critical care: No longer an oxymoron.

L12 ANSWER 2 OF 5 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 TI Traumatic carotid cavernous sinus fistula following a gunshot wound to the face.

L12 ANSWER 3 OF 5 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN DUPLICATE 1
 TI Starch accumulation during hydroponic growth of spinach and basil plants under carbon dioxide enrichment.

L12 ANSWER 4 OF 5 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 TI Starch accumulation during hydroponic growth of spinach and basil plants

under carbon dioxide enrichment.

- L12 ANSWER 5 OF 5 AGRICOLA Compiled and distributed by the National
Agricultural Library of the Department of Agriculture of the United States
of America. It contains copyrighted materials. All rights reserved.
(2004) on STN DUPLICATE 2
- TI Basil chlorosis: a physiological disorder in CO2-enriched atmospheres.